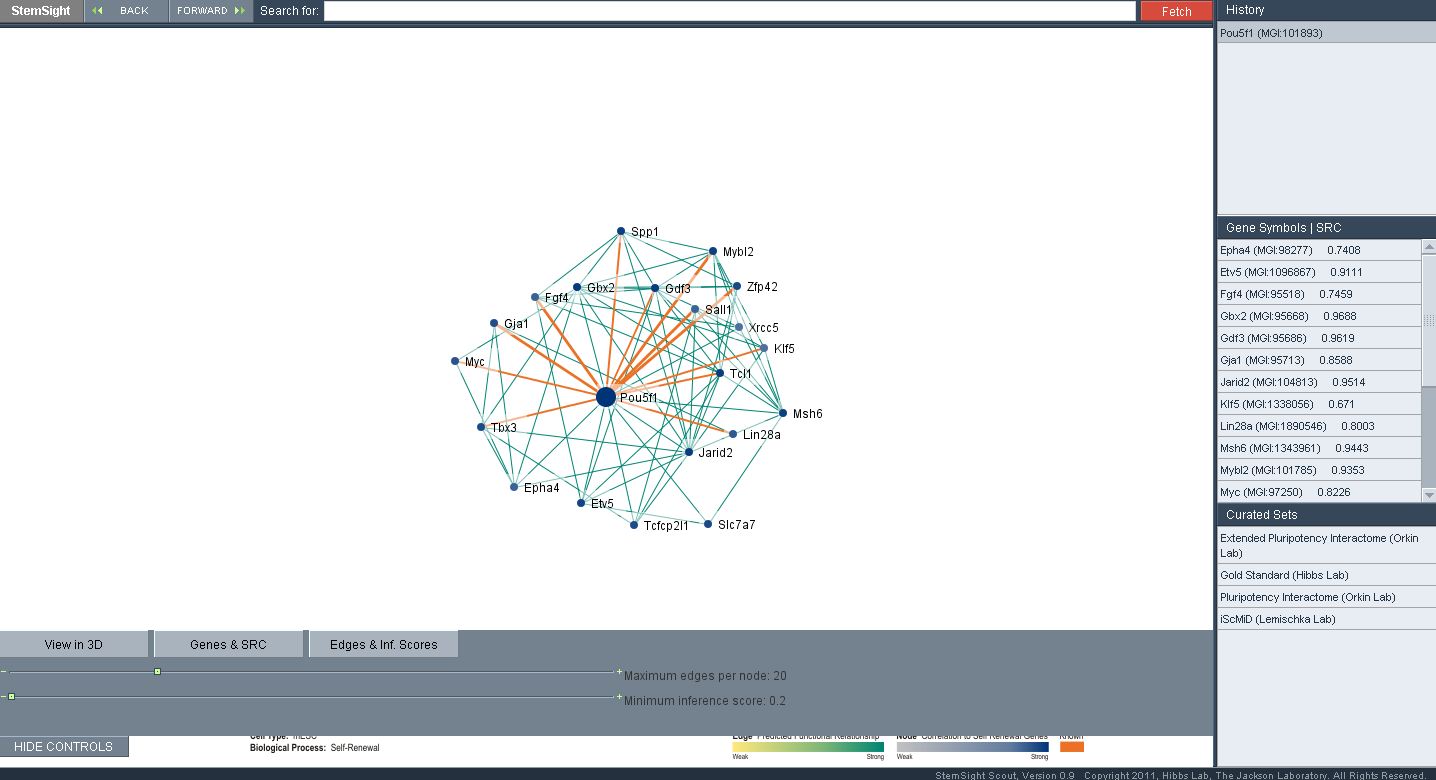
* Who designed the work and what was the intended audience?

StemSight Scout is a tool developed by the Jackson Laboratory that focuses their research on how to utilize high-throughput data sources to understand biology at multiple levels. They contend that the past decade has shown an increase in experimental techniques and resources, however, the rate at which data are translated into knowledge is progressing much slower than the rate of data generation. Thus, to help build connections, the lab specializes in the development of algorithms for the analysis, exploration, and visualization of data.StemSight scout allows for the exploration of potential similarities between genes. The underlying data merges information from literature with information taken from various experiments. Ultimately, researchers can quickly narrow their research to one specific gene for exploration which can further be examined in the lab and consequently allow for efficient experimentation. Since StemSight is public, other researchers can access the data which can help expedite solutions to be found. ­­

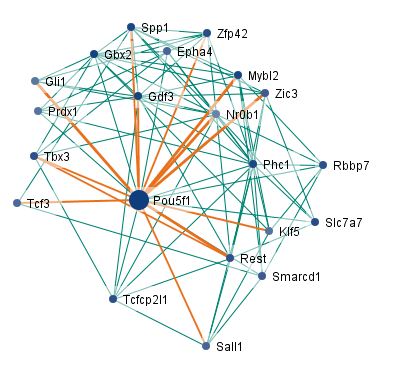
The StemSight scout visualization helps researchers discover information that might otherwise be difficult to explore without the visualization. The team led by Professor Matthew Hibbs study stem cells which are able to divide and differentiate into various cell types. The group’s interest lies in the process of ‘self-renewal’, as this process might contain the answers, for which, many scientists suspect is key to the understanding of how cancers form. With the discovery of the complete mouse and human genome, researchers have yet to discover what function the majority of these genes accomplish and or how they interact with each other. By combining known studies from literature with analysis from experiments, StemSight scout helps determine useful relationships. The output of one visual display shows two different types of relationships. Those that are known to be true, genes inferred to be functionally based on classical research, and those that have yet to be tested, based on inferences from over 800 different analyses used to determine similarities between genes. Based on probabilistic functional relationship, researchers can discover unusual genes and gene products that are likely related to a specific gene of interest.

Roam Gene Neighbourhoods

To begin, enter the official gene symbol for the gene of interest and press *Fetch.* StemSight scout will retrieve the genes inferred to be functionally related to the user’s gene of interest. Edge colour indicates the strength of the inferred functional relationship between genes. Node colour indicates a known documented relationship.

Access Edge and Node Details

Users can click on any edge to access detailed information on the strength of the predicted relationship between pairs of genes in the network and review datasets that support that edge. From the ‘edge detail’ window, the user can open the literature references in PubMed. As all data corresponds with literature substantiated by scholarly, peer reviewed journals, this may be one of the strongest assets of StemSight scout. After all, what good is data if there’s no credible source to back it up?

* How effective is the visualization at communicating its underlying data?

The gene **Pou5f1** plays a significant role in the self-renewal process. The **ORANGE** lines denote connections that are recognized from scientific literature. The **GREEN** lines denote connections that are ‘inferred’ from experimentation. Consequently, a researcher looking at the display might consider exploring gene Gbx2 to determine its role in the self-renewal process.

**Issues & Recommendation**

While the interface appears to be minimalist and simplistic in design, the developers opted to make the data visualization ‘hyper-dynamic’. Hence when the user initiates a new search, the visual is in constant movement until it settles into a static state. This not only wastes time, but can also have a dizzying effect The option to view in two-dimensionality and three- dimensionality had no functional purpose – if anything, the three dimensionality view appeared to be confusing to look at. Given that the visualization is intended for research purposes, the additional eye candy did more harm than good. During my exploration, StemSight scout had persistent glitches with the views control. During initial start-up, the page displays all controls for views at the bottom edge (View in 3D, Genes & SRC, Edges & Inf.) in addition to sliders that control edges per node and minimum inference score. If the user opted to hide controls and reactivate controls later, the sliders for the node and inference can no longer be seen. Additionally, when controls are not hidden, the legend for the Edge and Node is obstructed.

StemSight Scout is an effective tool for navigating through an abundance of data that can be used to explore and discover relationships between genes that can one day help find the cure for deseases.